

Supplemental Table S1. DNA Oligonucleotides

Name	Sequence (from 5' to 3')
G37	AATTGAATTCGGATCCCTAAGTCCAAC
G38	AATTGAATTCAGATCTCCCACTAGACAGC
G83	TTACAAAGTCACTCAGGATG
G1000	GTGCATCTGTCCAGTG
G1001	GCCGATTAGGTGACACTATAGAATACCCTGAAGTTCTC
G1009	GCCGATTAGGTGACACTATAGAATACTTAGCGTCTTCG
G1050	ATATGGTACCTCCACCATGGGCACCCCCGAG
G1051	TTAAGGATCCCAGCTCGCGCTG
G1052	ATATGAATTCAATGGATCTCTCTG
G1053	TTAACTCGAGCTACAGATCCTCTTCTG
G1120	ATTACTCGAGGCCGAGCAGAAC
G1121	ATATGTCGACCTATTCACTGACAG
G1576	GGAGGCCATGGAAGACGGTGAAAT
G1577	CCAAATCCTCCTCGGCCTCCTCTA
G1578	TAACATTGCTCCCCGGATTCTCAC
G1579	AGGTTGTAGCGATTCCCAGGTTCA
G1653	ATTAGGATCCCCTCCATCACA
G1654	TAATCTCGAGCTATTGCTTCATGGG

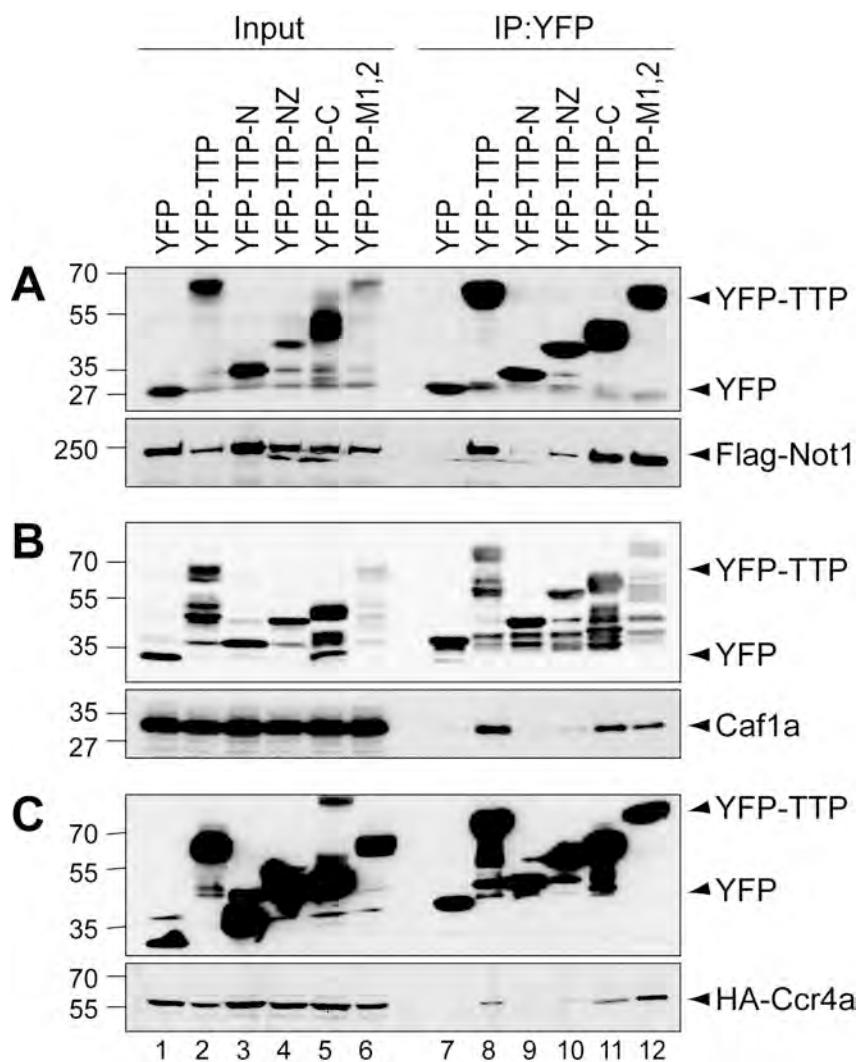
Supplemental Table S2. Proteins identified by mass spectrometry in GS-TTP purification

Symbol	Protein	kDa	GenID	Peptide coverage (%)	Peptide No GS	Peptide No GS-TTP
ACACB	acetyl-CoA carboxylase 2	277	32	9	0	7
CNOT1	CCR4-NOT complex subunit 1	267	23019	9	0	19
CPM	carboxypeptidase M	51	1368	25	0	11
ECHI	enoyl CoA hydratase 1, peroxysomal	36	1891	14	0	5
ELAVL1	RNA binding protein HuR	36	1994	10	0	3
EMD	emerin, nuclear lamina associated	29	2010	4	1	4
ENO1	enolase 1, alpha	47	2023	6	0	3
GIGYF1	GRB10 interacting GYF protein 1	115	64599	4	0	3
H1ST1H1D	Histone H1.3	22	3007	15	0	3
H1ST1H2BC	Histone H2B.1	14	8347	6	1	5
H1ST3H3	Histone H3t	16	8290	5	1	4
HNRNPH2	RNA binding protein hnRNP H2	49	3188	11	0	4
HNRNPA2B1	RNA binding protein hnRNP A2/B1	37	3181	10	0	3
HNRPC	RNA binding protein hnRNP C1/C2	34	3183	36	0	12
HNRNPUL1	RNA binding protein hnRNP U-like 1	96	11100	13	0	9
IGF2BP3	Insulin-like growth factor 2 mRNA binding protein 3	64	10643	13	0	7
MOV10	RNA helicase MOV10	114	4343	6	0	6

Supplemental Table S2 (continued). Proteins identified by mass spectrometry in GS-TTP purification

Symbol	Protein	kDa	GenID	Peptide coverage (%)	Peptide No GS	Peptide No GS-TTP
MRPL15	39S ribosomal protein L15, mitochondrial	33	29088	10	0	3
MRPL38	39S ribosomal protein L38, mitochondrial	45	6497	7	0	3
NCBP2	nuclear cap-binding protein subunit 2	18	22916	21	0	4
PABPC1	poly(A) binding protein, cytoplasmic 1	71	26986	16	0	9
PLOD1	procollagen lysyl hydroxylase	84	5351	29	0	18
RALY	RNA binding protein Raly	32	22913	21	0	5
RPS9	40S ribosomal protein S9	23	6203	13	0	3
SRRM2	RNA binding protein and splicing factor SRm300	300	23524	1	0	3
YBX1	Y-box binding protein YB1	36	4904	13	0	3
YWHA _B	14-3-3 protein beta	28	7529	39	0	5 (11)*
YWHA _E	14-3-3 protein epsilon	29	7531	44	1	15
YWHA _H	14-3-3 protein eta	28	7533	26	0	2 (7)*
YWHA _G	14-3-3 protein gamma	28	7532	40	0	10 (13)*
YWHA _Z	14-3-3 protein zeta	28	7534	35	0	3 (9)*
Zfp36	tristetraprolin	34	22695	33	0	12

* No of peptides that are not unique to the isoform are given in parentheses



Supplemental Figure S1. The C-terminal domain of TTP associates with Not1, Caf1a and Ccr4. (A) HEK293 cells were transiently transfected with YFP-tagged TTP constructs as indicated together with Flag-Not1. Cytoplasmic lysates (input) were prepared after 24 hours for immunoprecipitation (IP) with GFP-binder. Western blot analysis was carried out with antibodies against YFP and Flag. (B) Transfection and IP were carried out as above. Antibodies against YFP and endogenous Caf1a were used for Western blot analysis. (C) HEK293 cells were transiently transfected with YFP-tagged TTP constructs and HA-Ccr4a, and processed as above. Western blot analysis was carried out with antibodies against YFP and HA.